

1
SEQUENCE LISTING

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Collins, Jon

<120> CAR LIGAND-BINDING DOMAIN POLYPEPTIDE CO-CRYSTALLIZED WITH A
LIGAND, AND METHODS OF DESIGNING LIGANDS THAT MODULATE CAR
ACTIVITY

<130> PR60235

<150> 60/488,415
<151> 2003-07-18

<160> 7

<170> PatentIn version 3.2

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<213> Homo sapiens

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| agaggcattc cataccagat tctgtggcct gcaggtgaca tgctgcctaa gagaagcagg | 240 |
| agtctgtgac agccacccca acacgtgacg tc atg gcc agt agg gaa gat gag | 293 |
| Met Ala Ser Arg Glu Asp Glu | |
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| ctg agg aac tgt gtg gta tgt ggg gac caa gcc aca ggc tac cac ttt | 341 |
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| Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Val | |
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| Ser Lys Ser Ile Gly Pro Thr Cys Pro Phe Ala Gly Ser Cys Glu Val | |
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| Ser Lys Thr Gln Arg Arg His Cys Pro Ala Cys Arg Leu Gln Lys Cys | |
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| Ala | Leu | Arg | Arg | Ala | Lys | Gln | Ala | Gln | Arg | Arg | Ala | Gln | Gln | Thr | Pro | | |
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| gtg | caa | ctg | agt | aag | gag | caa | gaa | gag | ctg | atc | cgg | aca | ctc | ctg | ggg | 629 | |
| Val | Gln | Leu | Ser | Lys | Glu | Gln | Glu | Glu | Leu | Ile | Arg | Thr | Leu | Leu | Gly | | |
| | 105 | | | | | 110 | | | | | 115 | | | | | | |
| gcc | cac | acc | cgc | cac | atg | ggc | acc | atg | ttt | gaa | cag | ttt | gtg | cag | ttt | 677 | |
| Ala | His | Thr | Arg | His | Met | Gly | Thr | Met | Phe | Glu | Gln | Phe | Val | Gln | Phe | | |
| 120 | | | | | 125 | | | | | 130 | | | | | 135 | | |
| agg | cct | cca | gct | cat | ctg | ttc | atc | cat | cac | cag | ccc | ttg | ccc | acc | ctg | 725 | |
| Arg | Pro | Pro | Ala | His | Leu | Phe | Ile | His | His | Gln | Pro | Leu | Pro | Thr | Leu | | |
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| Ala | Pro | Val | Leu | Pro | Leu | Val | Thr | His | Phe | Ala | Asp | Ile | Asn | Thr | Phe | | |
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| atg | gta | ctg | caa | gtc | atc | aag | ttt | act | aag | gac | ctg | ccc | gtc | ttc | cgt | 821 | |
| Met | Val | Leu | Gln | Val | Ile | Lys | Phe | Thr | Lys | Asp | Leu | Pro | Val | Phe | Arg | | |
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| tcc | ctg | ccc | att | gaa | gac | cag | atc | tcc | ctt | ctc | aag | gga | gca | gct | gtg | 869 | |
| Ser | Leu | Pro | Ile | Glu | Asp | Gln | Ile | Ser | Leu | Leu | Lys | Gly | Ala | Ala | Val | | |
| | 185 | | | | | 190 | | | | | 195 | | | | | | |
| gaa | atc | tgt | cac | atc | gta | ctc | aat | acc | act | ttc | tgt | ctc | caa | aca | caa | 917 | |
| Glu | Ile | Cys | His | Ile | Val | Leu | Asn | Thr | Thr | Phe | Cys | Leu | Gln | Thr | Gln | | |
| 200 | | | | | 205 | | | | | 210 | | | | | 215 | | |
| aac | ttc | ctc | tgc | ggg | cct | ctt | cgc | tac | aca | att | gaa | gat | gga | gcc | cgt | 965 | |
| Asn | Phe | Leu | Cys | Gly | Pro | Leu | Arg | Tyr | Thr | Ile | Glu | Asp | Gly | Ala | Arg | | |
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| Val | Gly | Phe | Gln | Val | Glu | Phe | Leu | Glu | Leu | Leu | Phe | His | Phe | His | Gly | | |
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| Thr | Leu | Arg | Lys | Leu | Gln | Leu | Gln | Glu | Pro | Glu | Tyr | Val | Leu | Leu | Ala | | |
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| gag | att | gat | cag | ctg | caa | gag | gag | atg | gca | ctg | act | ctg | caa | agc | tac | 1157 | |
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| atc | aag | ggc | cag | cag | cga | agg | ccc | cgg | gat | cgg | ttt | ctg | tat | gcg | aag | 1205 | |
| Ile | Lys | Gly | Gln | Gln | Arg | Arg | Pro | Arg | Asp | Arg | Phe | Leu | Tyr | Ala | Lys | | |
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| ttg | cta | ggc | ctg | ctg | gct | gag | ctc | cgg | agc | att | aat | gag | gcc | tac | ggg | 1253 | |
| Leu | Leu | Gly | Leu | Leu | Ala | Glu | Leu | Arg | Ser | Ile | Asn | Glu | Ala | Tyr | Gly | | |
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 330 335 340

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 Gln Glu Ile Cys Ser
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Phe Ala Gly Ser Cys Glu Val Ser Lys Thr Gln Arg Arg His Cys Pro
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Ala Cys Arg Leu Gln Lys Cys Leu Asp Ala Gly Met Arg Lys Asp Met
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Ile Leu Ser Ala Glu Ala Leu Ala Leu Arg Arg Ala Lys Gln Ala Gln
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Arg Arg Ala Gln Gln Thr Pro Val Gln Leu Ser Lys Glu Gln Glu Glu
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Leu Ile Arg Thr Leu Leu Gly Ala His Thr Arg His Met Gly Thr Met
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Phe Glu Gln Phe Val Gln Phe Arg Pro Pro Ala His Leu Phe Ile His
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His Gln Pro Leu Pro Thr Leu Ala Pro Val Leu Pro Leu Val Thr His
 145 150 155 160

Phe Ala Asp Ile Asn Thr Phe Met Val Leu Gln Val Ile Lys Phe Thr
 165 170 175

4

Lys Asp Leu Pro Val Phe Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser
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Leu Leu Lys Gly Ala Ala Val Glu Ile Cys His Ile Val Leu Asn Thr
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Thr Phe Cys Leu Gln Thr Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr
 210 215 220

Thr Ile Glu Asp Gly Ala Arg Val Gly Phe Gln Val Glu Phe Leu Glu
 225 230 235 240

Leu Leu Phe His Phe His Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu
 245 250 255

Pro Glu Tyr Val Leu Leu Ala Ala Met Ala Leu Phe Ser Pro Asp Arg
 260 265 270

Pro Gly Val Thr Gln Arg Asp Glu Ile Asp Gln Leu Gln Glu Glu Met
 275 280 285

Ala Leu Thr Leu Gln Ser Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg
 290 295 300

Asp Arg Phe Leu Tyr Ala Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg
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Ser Ile Asn Glu Ala Tyr Gly Tyr Gln Ile Gln His Ile Gln Gly Leu
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48

ggg gcc cac acc cgc cac atg ggc acc atg ttt gaa cag ttt gtg cag

96

6

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 Gly Ala His Thr Arg His Met Gly Thr Met Phe Glu Gln Phe Val Gln
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 Phe Arg Pro Pro Ala His Leu Phe Ile His His Gln Pro Leu Pro Thr
 35 40 45
 Leu Ala Pro Val Leu Pro Leu Val Thr His Phe Ala Asp Ile Asn Thr
 50 55 60
 Phe Met Val Leu Gln Val Ile Lys Phe Thr Lys Asp Leu Pro Val Phe
 65 70 75 80
 Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala
 85 90 95
 Val Glu Ile Cys His Ile Val Leu Asn Thr Thr Phe Cys Leu Gln Thr
 100 105 110
 Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr Thr Ile Glu Asp Gly Ala
 115 120 125
 Arg Val Gly Phe Gln Val Glu Phe Leu Glu Leu Leu Phe His Phe His
 130 135 140
 Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu Pro Glu Tyr Val Leu Leu
 145 150 155 160
 Ala Ala Met Ala Leu Phe Ser Pro Asp Arg Pro Gly Val Thr Gln Arg
 165 170 175
 Asp Glu Ile Asp Gln Leu Gln Glu Glu Met Ala Leu Thr Leu Gln Ser
 180 185 190
 Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg Asp Arg Phe Leu Tyr Ala
 195 200 205
 Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg Ser Ile Asn Glu Ala Tyr
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 Gly Tyr Gln Ile Gln His Ile Gln Gly Leu Ser Ala Met Met
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 <223> Forward primer for amplifying amino acids 103-348, including sequences encoding a His tag, and including an NdeI restriction site

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 aaggagcaa 69

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 <212> DNA
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